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Amendments to Claims

**Claim 1. (Withdrawn)** A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

- a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;
  - 1) a promoter region of a gene selected from the group consisting of: a *nrtA* gene and a *glnB* gene; and
  - 2) a coding region of interest expressible in a C1 metabolizing bacteria; wherein the promoter region is operably linked to a coding region of interest; and
- b) growing the transformed C1 metabolizing bacteria cell of step (a) in the presence of nitrate wherein the chimeric gene is expressed.

**Claim 2. (Withdrawn)** A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

- a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;
  - 1) a promoter region of a *glyoxII* gene; and
  - 2) a coding region of interest expressible in a C1 metabolizing bacteria; wherein the promoter region is operably linked to a coding region of interest; and
- b) growing the transformed C1 metabolizing bacteria cell of step (a) at a pH of about 5.5 wherein the chimeric gene is expressed.

**Claim 3. (Withdrawn)** A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

- a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;
  - 1) a promoter region of a *htpG* gene; and
  - 2) a coding region of interest expressible in a C1 metabolizing bacteria; wherein the promoter region is operably linked to a coding region of interest; and
- b) growing the transformed C1 metabolizing bacteria cell of step (a) at a temperature suitable for induction of the promoter region wherein the chimeric gene is expressed.

**Claim 4. (Withdrawn)** A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

- a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;

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- 1) a promoter region of a gene selected from the group consisting of: a *moxF* gene and a *hps* gene; and
- 2) a coding region of interest expressible in a C1 metabolizing bacteria; wherein the promoter region is operably linked to a coding region of interest; and
- b) growing the transformed C1 metabolizing bacteria cell of step (a) in the presence of a C1 carbon source selected from the group consisting of methane and methanol wherein the chimeric gene of step (a) is expressed.

**Claim 5. (Withdrawn)** A method according to any of Claims 1-4 wherein the C1 metabolizing bacterial host cell is selected from the group consisting of methanotrophs and methylotrophs.

**Claim 6. (Withdrawn)** A method according to Claim 5 wherein the C1 metabolizing bacterial host cell is a methylotroph selected from the group consisting of *Methylomonas*, *Methylobacter*, *Methylococcus*, *Methylosinus*, *Methylocystis*, *Methylomicrobium*, *Methanomonas*, *Methylophilus*, *Methylobacillus*, *Methylobacterium*, *Hyphomicrobium*, *Xanthobacter*, *Bacillus*, *Paracoccus*, *Nocardia*, *Arthrobacter*, *Rhodopseudomonas*, and *Pseudomonas*.

**Claim 7. (Withdrawn)** A method according to Claim 1 wherein the promoter region has the nucleic acid sequence selected from the group consisting of SEQ ID NO:3 and SEQ ID NO:6.

**Claim 8. (Withdrawn)** A method according to Claim 2 wherein the promoter region has the nucleic acid sequence as set forth in SEQ ID NO:9.

**Claim 9. (Withdrawn)** A method according to Claim 3 wherein the promoter region has the nucleic acid sequence as set forth in SEQ ID NO:12.

**Claim 10. (Withdrawn)** A method according to Claim 3 wherein the temperature suitable for induction of the promoter region is selected from the group consisting of:

- a) 41-42°C wherein the C1 metabolizing bacteria is mesophilic; and
- b) 47-50°C wherein the C1 metabolizing bacteria, is thermophilic

**Claim 11. (Withdrawn)** A method according to Claim 4 wherein the nucleic acid fragment comprising the promoter region has the nucleic acid sequence selected from the group consisting of SEQ ID NO:15, and 18.

**Claim 12. (Withdrawn)** A method according to Claim 1 wherein the concentration of nitrate is from about 5mM to about 15mM.

**Claim 13. (Withdrawn)** The method according to any one of Claims 1 - 4 wherein the coding region of interest is selected from the group consisting of genes encoding: transaldolase, fructose bisphosphate aldolase, keto deoxy phosphogluconate aldolase, phosphoglucomutase, glucose-6-phosphate isomerase, phosphofructokinase, 6-phosphogluconate dehydratase, 6-phosphogluconate-6-phosphate-1 dehydrogenase, *dxs*, *dxr*, *ispA*, *ispD*, *ispE*, *ispF*, *crtE*, *crtX*, *crtY*, *crtI*, *crtB*, *crtZ*, *crtD*, *crtO*, *crtW*, genes encoding

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limonene synthase, *ugp*, *gumD*, *wza*, *espB*, *espM*, *waaE*, *espV*, *gumH*, genes encoding glycosyltransferase genes, *aroG*, *aroB*, *aroQ*, *aroE*, *aroK*, 5-enolpyruvylshikimate-3-phosphate synthase, *aroC*, *trpE*, *trpD*, *trpC*, *trpB*, *pheA*, *tyrAc*, *pds*, *phaC*, *phaE*, *efe*, *pdc*, *adh*, pinene synthase, bornyl synthase, phellandrene synthase, cineole synthase, sabinene synthase, and taxadiene synthase.

**Claim 14. (Withdrawn)** A method for the production of zeaxanthin comprising:

- a) providing a transformed C1 metabolizing host cell comprising:
  - 1) suitable levels of b-Carotene; and
  - 2) a chimeric gene comprising the promoter region of the *hps* gene operably linked to a coding region encoding  $\beta$ -carotene hydroxylase; and
- (b) contacting the host cell of step (a) under suitable growth conditions with an effective amount of a C1 carbon substrate whereby an zeaxanthin is produced.

**Claim 15. (Currently Amended).** An isolated nucleic acid molecule encoding a nitrate inducible gene selected from the group consisting of:

- (a) an isolated nucleic acid molecule encoding the amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:5;
- (b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC, 0.1% SDS, 65°C; or an isolated nucleic acid molecule that is complementary to (a), or (b).

**Claim 16. (Currently Amended).** The isolated nucleic acid molecule of Claim 15 ~~selected from the group consisting of as set forth in SEQ ID NO:1, and SEQ ID NO:4.~~

**Claim 17. (Withdrawn)** A polypeptide encoded by the isolated nucleic acid molecule of Claim 15.

**Claim 18. (Withdrawn)** The polypeptide of Claim 17 selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:5.

**Claim 19. (Currently Amended).** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a *nrtA* enzyme of at least 464 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:2;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 20. (Withdrawn)** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a *glnB* enzyme of at least 112 amino acids that has at least 76% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:5;

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or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 21. (Withdrawn)** An isolated nucleic acid molecule encoding a pH inducible gene selected from the group consisting of:

- a) an isolated nucleic acid molecule encoding the amino acid sequence as set forth in SEQ ID NO:8;
- b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC, 0.1% SDS, 65°C; or an isolated nucleic acid molecule that is complementary to (a), or (b).

**Claim 22. (Withdrawn)** The isolated nucleic acid molecule of Claim 21 as set forth in SEQ ID NO:7.

**Claim 23. (Withdrawn)** A polypeptide encoded by the isolated nucleic acid molecule of Claim 21.

**Claim 24. (Withdrawn)** The polypeptide of Claim 23 having the amino acid sequence as set forth in SEQ ID NO:8.

**Claim 25. (Withdrawn)** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a glyoxII enzyme of at least 231 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:8;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 26. (Withdrawn)** An isolated nucleic acid molecule encoding a temperature inducible gene selected from the group consisting of:

- a) an isolated nucleic acid molecule encoding the amino acid sequence as set forth in SEQ ID NO:11;
- b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC, 0.1% SDS, 65°C; or an isolated nucleic acid molecule that is complementary to (a), or (b).

**Claim 27. (Withdrawn)** The isolated nucleic acid molecule of Claim 26 as set forth in SEQ ID NO:10.

**Claim 28. (Withdrawn)** A polypeptide encoded by the isolated nucleic acid molecule of Claim 26.

**Claim 29. (Withdrawn)** The polypeptide of Claim 28 having the amino acid sequence as set forth in SEQ ID NO:11.

**Claim 30. (Withdrawn)** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a htpG enzyme of at least 644 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:11;

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or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 31. (Withdrawn)** An isolated nucleic acid molecule encoding a methane or methanol inducible gene selected from the group consisting of:

- (a) an isolated nucleic acid molecule encoding the amino acid sequence selected from the group consisting of SEQ ID NO:14, and 17;
- (b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC, 0.1% SDS, 65°C; or an isolated nucleic acid molecule that is complementary to (a), or (b).

**Claim 32. (Withdrawn)** The isolated nucleic acid molecule of Claim 31 selected from the group consisting of SEQ ID NO:13, and 16.

**Claim 33. (Withdrawn)** A polypeptide encoded by the isolated nucleic acid molecule of Claim 31.

**Claim 34. (Withdrawn)** The polypeptide of Claim 33 selected from the group consisting of SEQ ID NO:14, and 17.

**Claim 35. (Withdrawn)** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a *moxF* enzyme of at least 89 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:14;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 36. (Withdrawn)** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a *hps* enzyme of at least 215 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:17;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 37. (Withdrawn)** A promoter region responsive to the presence of nitrate having the nucleic acid sequence selected from the group consisting of SEQ ID NO:3 and SEQ ID NO:6.

**Claim 38. (Withdrawn)** A promoter region responsive to acidic pH having the nucleic acid sequence as set forth in SEQ ID NO:9.

**Claim 39. (Withdrawn)** A promoter region responsive to elevated temperatures having the nucleic acid sequence as set forth in SEQ ID NO:12.

**Claim 40. (Withdrawn)** A promoter region highly expressed in the presence of methane or methanol having the nucleic acid sequence selected from the group consisting of SEQ ID NO:15, and SEQ ID NO:18.

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